

DT05 Rec'd PCT/PTO 18 FEB 2005

1

## SEQUENCE LISTING

5 <110> SunGene GmbH & Co. KGaA

10 <120> Process for preparing ketocarotenoids in genetically modified organisms

15 <130> 20020636

<160> 74

20 <170> PatentIn version 3.1

25 <210> 1

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<212> DNA

30 <213> Nostoc sp. Strain PCC7120

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<221> CDS

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Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe

20 25 30

|    |   |     |
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|    | 'att gcc,tgc ttt atc tta ttt tta tgg gca att agt tta atc tta tta<br>Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu<br>35 40 45       | 144 |
| 5  | ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc<br>Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala<br>50 55 60        | 192 |
| 10 | atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat<br>Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His<br>65 70 75 80     | 240 |
| 15 | gat gcc atg cac ggc gta gtt tat ccc aaa aat ccc aga ata aat aat<br>Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn<br>85 90 95        | 288 |
| 20 | ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa<br>Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys<br>100 105 110     | 336 |
| 25 | gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat<br>Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp<br>115 120 125     | 384 |
| 30 | tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg<br>Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp<br>130 135 140     | 432 |
| 35 | tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga<br>Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly<br>145 150 155 160 | 480 |
| 40 | tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa<br>Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu<br>165 170 175     | 528 |
| 45 | aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta<br>Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val<br>180 185 190     | 576 |
| 50 | caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt<br>Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly<br>195 200 205     | 624 |
| 55 | ggt tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt<br>Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe<br>210 215 220     | 672 |
| 60 | tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac<br>Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His<br>225 230 235 240 | 720 |

gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata 768  
 Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile  
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Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu  
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Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala  
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Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
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10 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly  
 145 150 155 160

15 Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu  
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20 Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val  
 180 185 190

25 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly  
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30 Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe  
 210 215 220

35 Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His  
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|    | tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg att gtc ata gta | 96  |
|    | Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val |     |
|    | " 20 25 30  |     |
| 15 | att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat | 144 |
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|    | 35 40 45  |     |
| 20 | tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa | 192 |
|    | Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln |     |
|    | 50 55 60  |     |
|    | atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat | 240 |
| 25 | Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His |     |
|    | 65 70 75 80   |     |
|    | ggg tca gtt tat cgt aaa aat ccc aaa att aat dat ttt atc ggt tca | 288 |
| 30 | Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser |     |
|    | 85 90 95  |     |
|    | cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag | 336 |
|    | Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys |     |
|    | 100 105 110   |     |
| 35 | aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat | 384 |
|    | Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp |     |
|    | 115 120 125   |     |
| 40 | ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc | 432 |
|    | Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe |     |
|    | 130 135 140   |     |
|    | atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta | 480 |
| 45 | Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu |     |
|    | 145 150 155 160   |     |
|    | ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc | 528 |
|    | Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile |     |
| 50 | 165 170 175   |     |
|    | tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat | 576 |

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5 ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat 624  
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 195 200 205

10 ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc 672  
 Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile  
 210 215 220

15 gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat 720  
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 225 230 235 240

gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac 768  
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45 Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn  
 35 40 45

50 Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln  
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5 Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser  
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10 Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys  
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15 Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp  
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20 Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe  
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Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu  
 145 150 155 160

25 Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile  
 165 170 175

30 Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr  
 180 185 190

35 Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr  
 195 200 205

40 Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile  
 210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
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 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val  
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 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp  
 35 40 45  
 35 atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa 192  
 Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln  
 50 55 60  
 aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240  
 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His  
 40 65 70 75 80  
 ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca 288  
 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr  
 85 90 95  
 45 ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa 336  
 Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys  
 100 105 110  
 50 aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat 384  
 Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp  
 115 120 125



ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt 432  
 Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe  
 130 135 140

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atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att 480  
 Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile  
 145 150 155 160

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tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act 528  
 Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr  
 165 170 175

15

tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta' caa tta' ttc tat 576  
 Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
 180 185 190

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ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag 624  
 Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
 195 200 205

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cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc 672  
 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
 210 215 220

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 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
 225 230 235 240

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 20 25 30

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|    | Ile | Val | Ser | Ala | Trp | Val | Ile | Ser | Leu | Ser | Leu | Leu | Leu | Ser | Leu | Asp |  |
|    |     |     | 35  |     |     |     |     |     | 40  |     |     |     |     |     |     | 45  |  |
| 5  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Ile | Ser | Lys | Leu | Lys | Phe | Trp | Met | Leu | Leu | Pro | Val | Ile | Leu | Trp | Gln |  |
|    |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| 10 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Thr | Phe | Leu | Tyr | Thr | Gly | Leu | Phe | Ile | Thr | Ser | His | Asp | Ala | Met | His |  |
|    | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| 15 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Gly | Val | Val | Phe | Pro | Gln | Asn | Thr | Lys | Ile | Asn | His | Leu | Ile | Gly | Thr |  |
|    |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| 20 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Leu | Thr | Leu | Ser | Leu | Tyr | Gly | Leu | Leu | Pro | Tyr | Gln | Lys | Leu | Leu | Lys |  |
|    |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| 25 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Lys | His | Trp | Leu | His | His | His | Asn | Pro | Ala | Ser | Ser | Ile | Asp | Pro | Asp |  |
|    |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| 30 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Phe | His | Asn | Gly | Lys | His | Gln | Ser | Phe | Phe | Ala | Trp | Tyr | Phe | His | Phe |  |
|    |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| 35 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Met | Lys | Gly | Tyr | Trp | Ser | Trp | Gly | Gln | Ile | Ile | Ala | Leu | Thr | Ile | Ile |  |
|    | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| 40 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Tyr | Phe | Trp | Val | Leu | Pro | Ser | Leu | Leu | Ser | Ser | Leu | Gln | Leu | Phe | Tyr |  |
|    |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| 45 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Phe | Gly | Thr | Phe | Leu | Pro | His | Ser | Glu | Pro | Ile | Gly | Gly | Tyr | Val | Gln |  |
|    |     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| 50 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Pro | His | Cys | Ala | Gln | Thr | Ile | Ser | Arg | Pro | Ile | Trp | Trp | Ser | Phe | Ile |  |
|    |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| 55 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|    | Thr | Cys | Tyr | His | Phe | Gly | Tyr | His | Glu | Glu | His | His | Glu | Tyr | Pro | His |  |
|    | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys  
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&lt;211&gt; 789

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&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

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&lt;222&gt; (1)..(789)

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15

tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg att gtc ata gta 96

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val

20

25

30

35

att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat 144

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn

35

40

45

40

tat gcc aaa att cat aag tgg ttg ata cct att gca ata gtt tgg caa 192

Tyr Ala Lys Ile His Lys Trp Leu Ile Pro Ile Ala Ile Val Trp Gln

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55

60

atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat 240

45

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His

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ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca 288

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Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser

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95

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15 Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn  
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Tyr Ala Lys Ile His Lys Trp Leu Ile Pro Ile Ala Ile Val Trp Gln  
 50 55 60

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 65 70 75 80

25 Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser  
 85 90 95

30 Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys  
 100 105 110

35 Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp  
 115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe  
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40 Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu  
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45 Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile  
 165 170 175

50 Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr  
 180 185 190

14

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr  
 195 200 205

5 Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile  
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10 Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
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Asn Ser Val Thr Asn Ser  
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 Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn  
 35 40 45

|    |   |     |
|----|---|-----|
|    | tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa | 192 |
|    | Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln |     |
|    | 50 55 60  |     |
| 5  | atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat | 240 |
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|    | 65 70 75 80   |     |
| 10 | ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca | 288 |
|    | Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser |     |
|    | 85 90 95  |     |
|    | cta gct gta geg ctt tac gct gtg ttt cca tat caa cag atg tta aag | 336 |
| 15 | Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys |     |
|    | 100 105 110   |     |
|    | aat cat tgc tta cat cat cgt cat cct gct agc gat tta gac cca gat | 384 |
|    | Asn His Cys Leu His His Arg His Pro Ala Ser Asp Leu Asp Pro Asp |     |
| 20 | 115 120 125   |     |
|    | ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc | 432 |
|    | Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe |     |
|    | 130 135 140   |     |
| 25 | atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta | 480 |
|    | Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu |     |
|    | 145 150 155 160   |     |
| 30 | ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc | 528 |
|    | Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile |     |
|    | 165 170 175   |     |
|    | tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat | 576 |
| 35 | Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr |     |
|    | 180 185 190   |     |
|    | ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat | 624 |
|    | Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr |     |
| 40 | 195 200 205   |     |
|    | ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc | 672 |
|    | Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile |     |
|    | 210 215 220   |     |
| 45 | gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat | 720 |
|    | Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His |     |
|    | 225 230 235 240   |     |
| 50 | gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac | 768 |
|    | Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn |     |
|    | 245 250 255   |     |

'aat tca, gta acc aat tcg taa  
 Asn Ser Val Thr Asn Ser  
 260

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<210> 10

<211> 262

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<212> PRT

<213> Artificial sequence

15

<400> 10

20 Met Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln  
 1 5 10 15

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val  
 20 25 30

25

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn  
 35 40 45

30

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln  
 50 55 60

35 Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His  
 65 70 75 80

40 Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser  
 85 90 95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys  
 100 105 110

45

Asn His Cys Leu His His Arg His Pro Ala Ser Asp Leu Asp Pro Asp  
 115 120 125

50

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe  
 130 135 140



Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu  
145 150 155 160

5

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile  
165 170 175

10

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr  
180 185 190

15

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr  
195 200 205

20

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile  
210 215 220

25

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
225 230 235 240

30

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn  
245 250 255

35

Asn Ser Val Thr Asn Ser  
260

40

<210> 11

<211> 762

<212> DNA

<213> Artificial sequence

45

<220>

<221> CDS

<222> (1)..(762)

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<223>

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 5 Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro  
 1 5 10 15

gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96  
 10 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val  
 20 25 30

att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144  
 15 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp  
 35 40 45

atc tca aag att cat aag tgg atg tta ttg cct gtt ata cta tgg caa 192  
 Ile Ser Lys Ile His Lys Trp Met Leu Leu Pro Val Ile Leu Trp Gln  
 50 55 60

aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240  
 20 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His  
 65 70 75 80

ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca 288  
 25 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr  
 85 90 95

ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa 336  
 30 Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys  
 100 105 110

aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat 384  
 35 Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp  
 115 120 125

ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt 432  
 Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe  
 130 135 140

atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att 480  
 40 Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile  
 145 150 155 160

tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act 528  
 45 Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr  
 165 170 175

tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat 576  
 50 Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
 180 185 190

ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag 624

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
 195 200 205

5 cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc 672  
 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
 210 215 220

10 acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat 720  
 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
 225 230 235 240

15 att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag 762  
 Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys  
 245 250

<210> 12

20 <211> 253  
 <212> PRT  
 <213> Artificial sequence

25 <400> 12

30 Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro  
 1 5 10 15

35 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val  
 20 25 30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp  
 35 40 45

40 Ile Ser Lys Ile His Lys Trp Met Leu Leu Pro Val Ile Leu Trp Gln  
 50 55 60

45 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His  
 65 70 75 80

50 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr  
 85 90 95

## 20

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys  
 100 105 110

5 Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp  
 115 120 125

10 Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe  
 130 135 140

15 Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile  
 145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr  
 165 170 175

20 Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
 180 185 190

25 Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
 195 200 205

30 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
 210 215 220

35 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
 225 230 235 240

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys  
 245 250

40 <210> 13  
 <211> 762

45 <212> DNA  
 <213> Artificial sequence

50 <220>

&lt;221&gt; CDS

&lt;222&gt; (1)..(762)

5 &lt;223&gt;

&lt;400&gt; 13

|    |   |     |
|----|---|-----|
| 10 | atg atc cag tta gaa caa cca ctc agt cat caa gca aaa ctg act cca | 48  |
|    | Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro |     |
|    | 1 5 10 15   |     |
| 15 | gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc | 96  |
|    | Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val |     |
|    | 20 25 30  |     |
| 20 | att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac | 144 |
|    | Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp     |     |
|    | 35 40 45  |     |
| 25 | atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa | 192 |
|    | Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln |     |
|    | 50 55 60  |     |
| 30 | aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat | 240 |
|    | Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His |     |
|    | 65 70 75 80   |     |
| 35 | ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca | 288 |
|    | Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr |     |
|    | 85 90 95  |     |
| 40 | ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa | 336 |
|    | Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys |     |
|    | 100 105 110   |     |
| 45 | aaa cat tgg tta cac cac cac aat cca gca agc gat tta gac ccg gat | 384 |
|    | Lys His Trp Leu His His His Asn Pro Ala Ser Asp Leu Asp Pro Asp |     |
|    | 115 120 125   |     |
| 50 | ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt | 432 |
|    | Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe |     |
|    | 130 135 140   |     |
| 55 | atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att | 480 |
|    | Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile |     |
|    | 145 150 155 160   |     |
| 60 | tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act | 528 |
|    | Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr |     |
|    | 165 170 175   |     |

5    'tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat    576  
      Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
              180                                185                                190

10    ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag    624  
      Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
              195                                200                                205

15    cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc    672  
      Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
              210                                215                                220

20    acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat    720  
      Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
              225                                230                                235                                240

25    att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag    762  
      Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys  
              245                                250

30    <210> 14  
      <211> 253  
      <212> PRT  
      <213> Artificial sequence

35    Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro  
      1                                5                                10                                15

40    Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val  
              20                                25                                30

45    Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp  
              35                                40                                45

50    Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln  
              50                                55                                60

55    Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His  
      65                                70                                75                                80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr  
 85 90 95  
 5  
 Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys  
 100 105 110  
 10  
 Lys His Trp Leu His His His Asn Pro Ala Ser Asp Leu Asp Pro Asp  
 115 120 125  
 15  
 Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe  
 130 135 140  
 20  
 Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile  
 145 150 155 160  
 Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr  
 165 170 175  
 25  
 Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
 180 185 190  
 30  
 Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
 195 200 205  
 35  
 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
 210 215 220  
 40  
 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
 225 230 235 240  
 Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys  
 245 250  
 45  
 <210> 15  
 <211> 1608  
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 <212> DNA

&lt;213&gt; Haematococcus pluvialis

5 &lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3)..(971)

10

&lt;223&gt;

15 &lt;400&gt; 15

ct aca ttt cac aag ccc gtg agc ggt gca agc gct ctg ccc cac atc 47  
 Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile  
 1 5 10 15

20 ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95  
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu  
 20 25 30

25 tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc 143  
 Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala  
 35 40 45

30 cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg 191  
 Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser  
 50 55 60

35 tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga 239  
 Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly  
 65 70 75

acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca 287  
 Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala  
 80 85 90 95

40 ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa 335  
 Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys  
 100 105 110

45 cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc 383  
 Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly  
 115 120 125

50 gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac 431  
 Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His  
 130 135 140

atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc 479



25

Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu  
 145 150 155

5 ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat 527  
 Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr  
 160 165 170 175

10 gca cac aaa gcc atc tgg cat gag tcg cct ctg ggc tgg ctg ctg cac 575  
 Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His  
 180 185 190

15 aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg 623  
 Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu  
 195 200 205

ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc 671  
 Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly  
 210 215 220

20 ttc tgg ctg ccc aac qtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg 719  
 Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu  
 225 230 235

25 ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg 767  
 Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu  
 240 245 250 255

30 gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg 815  
 Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met  
 260 265 270

35 aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt 863  
 Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly  
 275 280 285

ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att 911  
 Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile  
 290 295 300

40 cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg 959  
 Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp  
 305 310 315

45 tcc aag cgg tag ggtgcggaac caggcacgct ggtttcacac ctcatgcctg 1011  
 Ser Lys Arg  
 320

tgataagggtg tggctagagc gatgcgtgtg agacgggtat gtcacggtcg actggtctga 1071

50 tggccaatgg catcggccat gtctggtcat cacgggctgg ttgcctgggt gaaggtgatg 1131

cacatcatca tgtgcggttg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc 1191

5 'caggctggcg ttgaatcagt gagggtttgt gattggcggt tgtgaagcaa tgactccgcc 1251  
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 'gtgcagcaaa ctatattcac ctagggtgtg ttgtaggatac aggtgaggcc ttgcacattg 1371  
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 10 agacgtagac cttgactgga ggcttgatcg agagagtggg ccgtattctt tgagagggga 1491  
 ggctcgtgcc agaaatggtg agtggatgac tgtgacgctg tacattgcag gcaggtgaga 1551  
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 20 <212> PRT  
 <213> Haematococcus pluvialis  
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 30 1 5 10 15  
 Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu Ser  
 35 20 25 30  
 Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala Arg  
 40 35 40 45  
 Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu  
 50 55 60  
 45 Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr  
 65 70 75 80  
 Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu  
 50 85 90 95

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg  
 100 105 110

5 Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val  
 115 120 125

10 Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met  
 130 135 140

15 Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu  
 145 150 155 160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala  
 165 170 175

20 His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys  
 180 185 190

25 Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe  
 195 200 205

30 Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe  
 210 215 220

35 Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly  
 225 230 235 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val  
 245 250 255

40 His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys  
 260 265 270

45 Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly  
 275 280 285

50 Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro  
 290 295 300

Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser  
 '305 310 315 320

5 Lys Arg

10 <210> 17

<211> 1650

<212> DNA

15 <213> Lycopersicon esculentum

20 <220>

<221> CDS

<222> (112)..(1614)

25 <223>

30 <400> 17  
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aggaccccat ttgaagtttt cttgaaacaa atattaccct gftggaaaaa g atg gat 117  
 Met Asp  
 1

35 " 165  
 act ttg ttg aaa acc cca aat aac ctt gaa ttt ctg aac cca cat cat  
 Thr Leu Leu Lys Thr Pro Asn Asn Leu Glu Phe Leu Asn Pro His His  
 5 10 15

40 ggt ttt gct gtt aaa gct agt acc ttt aga tct gag aag cat cat aat 213  
 Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His His Asn  
 20 25 30

45 ttt ggt tct agg aag ttt tgt gaa act ttg ggt aga agt gtt tgt gtt 261  
 Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val Cys Val  
 35 40 45 50

50 aag ggt agt agt agt gct ctt tta gag ctt gta cct gag acc aaa aag 309  
 Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr Lys Lys  
 55 60 65

gag aat ctt gat ttt gag ctt cct atg tat gac cct tca aaa ggg gtt 357

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|    | Glu | Asn | Leu | Asp | Phe | Glu | Leu | Pro | Met | Tyr | Asp | Pro | Ser | Lys | Gly | Val |     |
|    |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |     |     |
| 5  | gtt | gtg | gat | ctt | gct | gtg | gtt | ggt | ggt | ggc | cct | gca | gga | ctt | gct | gtt | 405 |
|    | Val | Val | Asp | Leu | Ala | Val | Val | Gly | Gly | Gly | Pro | Ala | Gly | Leu | Ala | Val |     |
|    |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |
| 10 | gca | cag | caa | gtt | tct | gaa | gca | gga | ctc | tct | gtt | tgt | tca | att | gat | ccg | 453 |
|    | Ala | Gln | Gln | Val | Ser | Glu | Ala | Gly | Leu | Ser | Val | Cys | Ser | Ile | Asp | Pro |     |
|    |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |
| 15 | aat | cct | aaa | ttg | ata | tgg | cct | aat | aac | tat | ggt | gtt | tgg | gtg | gat | gaa | 501 |
|    | Asn | Pro | Lys | Leu | Ile | Trp | Pro | Asn | Asn | Tyr | Gly | Val | Trp | Val | Asp | Glu |     |
|    | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |
| 20 | ttt | gag | gct | atg | gac | ttg | tta | gat | tgt | cta | gat | gct | acc | tgg | tct | ggt | 549 |
|    | Phe | Glu | Ala | Met | Asp | Leu | Leu | Asp | Cys | Leu | Asp | Ala | Thr | Trp | Ser | Gly |     |
|    |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     | 145 |     |     |
| 25 | gca | gca | gtg | tac | att | gat | gat | aat | acg | gct | aaa | gat | ctt | cat | aga | cct | 597 |
|    | Ala | Ala | Val | Tyr | Ile | Asp | Asp | Asn | Thr | Ala | Lys | Asp | Leu | His | Arg | Pro |     |
|    |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |     |
| 30 | tat | gga | agg | gtt | aac | cgg | aaa | cag | ctg | aaa | tcg | aaa | atg | atg | cag | aaa | 645 |
|    | Tyr | Gly | Arg | Val | Asn | Arg | Lys | Gln | Leu | Lys | Ser | Lys | Met | Met | Gln | Lys |     |
|    |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     |
| 35 | tgt | ata | atg | aat | ggt | gtt | aaa | ttc | cac | caa | gcc | aaa | gtt | ata | aag | gtg | 693 |
|    | Cys | Ile | Met | Asn | Gly | Val | Lys | Phe | His | Gln | Ala | Lys | Val | Ile | Lys | Val |     |
|    |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |
| 40 | att | cat | gag | gaa | tcg | aaa | tcc | atg | ttg | ata | tgc | aat | gat | ggt | aft | act | 741 |
|    | Ile | His | Glu | Glu | Ser | Lys | Ser | Met | Leu | Ile | Cys | Asn | Asp | Gly | Ile | Thr |     |
|    | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |
| 45 | att | cag | gca | acg | gtg | gtg | ctc | gat | gca | act | ggc | ttc | tct | aga | tct | ctt | 789 |
|    | Ile | Gln | Ala | Thr | Val | Val | Leu | Asp | Ala | Thr | Gly | Phe | Ser | Arg | Ser | Leu |     |
|    |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     | 225 |     |     |
| 50 | gtt | cag | tat | gat | aag | cct | tat | aac | ccc | ggg | tat | caa | gtt | gct | tat | ggc | 837 |
|    | Val | Gln | Tyr | Asp | Lys | Pro | Tyr | Asn | Pro | Gly | Tyr | Gln | Val | Ala | Tyr | Gly |     |
|    |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |     |     |
| 55 | att | ttg | gct | gaa | gtg | gaa | gag | cac | ccc | ttt | gat | gta | aac | aag | atg | gtt | 885 |
|    | Ile | Leu | Ala | Glu | Val | Glu | Glu | His | Pro | Phe | Asp | Val | Asn | Lys | Met | Val |     |
|    |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |     |
| 60 | ttc | atg | gat | tgg | cga | gat | tct | cat | ttg | aag | aac | aat | act | gat | ctc | aag | 933 |
|    | Phe | Met | Asp | Trp | Arg | Asp | Ser | His | Leu | Lys | Asn | Asn | Thr | Asp | Leu | Lys |     |
|    |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |
| 65 | gag | aga | aat | agt | aga | ata | cca | act | ttt | ctt | tat | gca | atg | cca | ttt | tca | 981 |

30

|      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
|      | Glu | Arg | Asn | Ser | Arg | Ile | Pro | Thr | Phe | Leu | Tyr | Ala | Met | Pro | Phe | Ser |      |
| '275 |     |     |     |     |     | 280 |     |     |     | 285 |     |     |     |     |     | 290 |      |
|      | tcc | aac | agg | ata | ttt | ctt | gaa | gaa | aca | tca | ctc | gta | gct | cgt | cct | ggc | 1029 |
| 5    | Ser | Asn | Arg | Ile | Phe | Leu | Glu | Glu | Thr | Ser | Leu | Val | Ala | Arg | Pro | Gly |      |
|      |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     | 305 |     |      |
|      | ttg | cgt | ata | gat | gat | att | caa | gaa | cga | atg | gtg | gct | cgt | tta | aac | cat | 1077 |
| 10   | Leu | Arg | Ile | Asp | Asp | Ile | Gln | Glu | Arg | Met | Val | Ala | Arg | Leu | Asn | His |      |
|      |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |      |
|      | ttg | ggg | ata | aaa | gtg | aag | agc | att | gaa | gaa | gat | gaa | cat | tgt | cta | ata | 1125 |
| 15   | Leu | Gly | Ile | Lys | Val | Lys | Ser | Ile | Glu | Glu | Asp | Glu | His | Cys | Leu | Ile |      |
|      |     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
|      | cca | atg | ggg | ggg | cca | ctt | cca | gta | tta | cct | cag | aga | gtc | gtt | gga | atc | 1173 |
| 20   | Pro | Met | Gly | Gly | Pro | Leu | Pro | Val | Leu | Pro | Gln | Arg | Val | Val | Gly | Ile |      |
|      |     |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |      |
|      | ggg | ggg | aca | gct | ggc | atg | gtt | cat | cca | tcc | acc | ggg | tat | atg | gtg | gca | 1221 |
| 25   | Gly | Gly | Thr | Ala | Gly | Met | Val | His | Pro | Ser | Thr | Gly | Tyr | Met | Val | Ala |      |
|      |     |     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |      |
|      | agg | aca | cta | gct | gcg | gct | cct | gtt | gtt | gcc | aat | gcc | ata | att | caa | tac | 1269 |
| 30   | Arg | Thr | Leu | Ala | Ala | Ala | Pro | Val | Val | Ala | Asn | Ala | Ile | Ile | Gln | Tyr |      |
|      |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     | 385 |     |      |
|      | ctc | ggg | tct | gaa | aga | agt | cat | tcg | ggg | aat | gaa | tta | tcc | aca | gct | gtt | 1317 |
| 35   | Leu | Gly | Ser | Glu | Arg | Ser | His | Ser | Gly | Asn | Glu | Leu | Ser | Thr | Ala | Val |      |
|      |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |     |      |
|      | tgg | aaa | gat | ttg | tgg | cct | ata | gag | agg | aga | cgt | caa | aga | gag | ttc | ttc | 1365 |
| 40   | Trp | Lys | Asp | Leu | Trp | Pro | Ile | Glu | Arg | Arg | Arg | Gln | Arg | Glu | Phe | Phe |      |
|      |     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
|      | tgc | ttc | ggg | atg | gat | att | ctt | ctg | aag | ctt | gat | tta | cct | gct | aca | aga | 1413 |
| 45   | Cys | Phe | Gly | Met | Asp | Ile | Leu | Leu | Lys | Leu | Asp | Leu | Pro | Ala | Thr | Arg |      |
|      |     |     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |      |
|      | agg | ttc | ttt | gat | gca | ttc | ttt | gac | tta | gaa | cct | cgt | tat | tgg | cat | ggc | 1461 |
| 50   | Arg | Phe | Phe | Asp | Ala | Phe | Phe | Asp | Leu | Glu | Pro | Arg | Tyr | Trp | His | Gly |      |
|      |     |     |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |      |
|      | ttc | tta | tcg | tct | cga | ttg | ttt | cta | cct | gaa | ctc | ata | gtt | ttt | ggg | ctg | 1509 |
| 55   | Phe | Leu | Ser | Ser | Arg | Leu | Phe | Leu | Pro | Glu | Leu | Ile | Val | Phe | Gly | Leu |      |
|      |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |     |      |
|      | tct | cta | ttc | tct | cat | gct | tca | aat | act | tct | aga | ttt | gag | ata | atg | aca | 1557 |
| 60   | Ser | Leu | Phe | Ser | His | Ala | Ser | Asn | Thr | Ser | Arg | Phe | Glu | Ile | Met | Thr |      |
|      |     |     |     |     | 470 |     |     |     |     | 475 | </  |     |     |     |     |     |      |

Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu Gln Asp  
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1650

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25 His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His  
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30 His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val  
 35 40 45

35 Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr  
 50 55 60

Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys  
 65 70 75 80

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Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu  
 85 90 95

45 Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile  
 100 105 110

50 Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val  
 115 120 125

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|    | Asp | Glu | Phe | Glu | Ala | Met | Asp | Leu | Leu | Asp | Cys | Leu | Asp | Ala | Thr | Trp |  |
|    | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| 5  | Ser | Gly | Ala | Ala | Val | Tyr | Ile | Asp | Asp | Asn | Thr | Ala | Lys | Asp | Leu | His |  |
|    | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| 10 | Arg | Pro | Tyr | Gly | Arg | Val | Asn | Arg | Lys | Gln | Leu | Lys | Ser | Lys | Met | Met |  |
|    |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| 15 | Gln | Lys | Cys | Ile | Met | Asn | Gly | Val | Lys | Phe | His | Gln | Ala | Lys | Val | Ile |  |
|    |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |  |
| 20 | Lys | Val | Ile | His | Glu | Glu | Ser | Lys | Ser | Met | Leu | Ile | Cys | Asn | Asp | Gly |  |
|    |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| 25 | Ile | Thr | Ile | Gln | Ala | Thr | Val | Val | Leu | Asp | Ala | Thr | Gly | Phe | Ser | Arg |  |
|    | 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| 30 | Ser | Leu | Val | Gln | Tyr | Asp | Lys | Pro | Tyr | Asn | Pro | Gly | Tyr | Gln | Val | Ala |  |
|    | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| 35 | Tyr | Gly | Ile | Leu | Ala | Glu | Val | Glu | Glu | His | Pro | Phe | Asp | Val | Asn | Lys |  |
|    |     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| 40 | Met | Val | Phe | Met | Asp | Trp | Arg | Asp | Ser | His | Leu | Lys | Asn | Asn | Thr | Asp |  |
|    |     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| 45 | Leu | Lys | Glu | Arg | Asn | Ser | Arg | Ile | Pro | Thr | Phe | Leu | Tyr | Ala | Met | Pro |  |
|    |     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| 50 | Phe | Ser | Ser | Asn | Arg | Ile | Phe | Leu | Glu | Glu | Thr | Ser | Leu | Val | Ala | Arg |  |
|    | 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| 55 | Pro | Gly | Leu | Arg | Ile | Asp | Asp | Ile | Gln | Glu | Arg | Met | Val | Ala | Arg | Leu |  |
|    | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| 60 | Asn | His | Leu | Gly | Ile | Lys | Val | Lys | Ser | Ile | Glu | Glu | Asp | Glu | His | Cys |  |
|    |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |



Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val  
 340 345 350

5 Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met  
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10 Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile  
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15 Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr  
 385 390 395 400

20 Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu  
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Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala  
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25 Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp  
 435 440 445

30 His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe  
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35 Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile  
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25 cgcaaatttt cggattagtg atgatttttc atggacttaa aaatctggtg catataccag 540  
aaaataattt aattatattt tggatgatac cttctatttt aagttcagta caactatttt 600  
30 attttggtag atttttgcct cataaaaagc tagaaggtgg ttatactaac cccattgtg 660  
cgcgcatgat cccattacct ctttttgggt cttttgttac ttgttatcac ttcggctacc 720  
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agcggct atg caa ccg cat tat gat ctg att ctc gtg ggg gct gga ctc 169

Met Gln Pro His Tyr Asp Leu Ile Leu Val Gly Ala Gly Leu

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Ala Asn Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln Gln Pro Asp Met

15 20 25 30

45 cgt att ttg ctt atc gac gcc gca ccc cag gcg ggc ggg aat cat acg 265

Arg Ile Leu Leu Ile Asp Ala Ala Pro Gln Ala Gly Gly Asn His Thr

35 40 45

50 tgg tca ttt cac cac gat gat ttg act gag agc caa cat cgt tgg ata 313

Trp Ser Phe His His Asp Asp Leu Thr Glu Ser Gln His Arg Trp Ile

50 55 60

|    |   |     |
|----|---|-----|
|    | gct ccg ctg gtg gtt cat cac tgg ccc gac tat cag gta cgc ttt ccc | 361 |
|    | Ala Pro Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro |     |
|    | 65 70 75  |     |
| 5  | aca cgc cgt cgt aag ctg aac agc ggc tac ttt tgt att act tct cag | 409 |
|    | Thr Arg Arg Arg Lys Leu Asn Ser Gly Tyr Phe Cys Ile Thr Ser Gln |     |
|    | 80 85 90  |     |
| 10 | cgt ttc gct gag gtt tta cag cga cag ttt ggc ccg cac ttg tgg atg | 457 |
|    | Arg Phe Ala Glu Val Leu Gln Arg Gln Phe Gly Pro His Leu Trp Met |     |
|    | 95 100 105 110  |     |
| 15 | gat acc gcg gtc gca gag gtt aat gcg gaa tct gtt cgg ttg aaa aag | 505 |
|    | Asp Thr Ala Val Ala Glu Val Asn Ala Glu Ser Val Arg Leu Lys Lys |     |
|    | 115 120 125   |     |
| 20 | ggc cag gtt atc ggt gcc cgc gcg gtg att gac ggg cgg ggt tat gcg | 553 |
|    | Gly Gln Val Ile Gly Ala Arg Ala Val Ile Asp Gly Arg Gly Tyr Ala |     |
|    | 130 135 140   |     |
| 25 | gca aat tca gca ctg agc gtg ggc ttc cag gcg ttt att ggc cag gaa | 601 |
|    | Ala Asn Ser Ala Leu Ser Val Gly Phe Gln Ala Phe Ile Gly Gln Glu |     |
|    | 145 150 155   |     |
| 30 | tgg cga ttg agc cac ccg cat ggt tta tcg tct ccc att atc atg gat | 649 |
|    | Trp Arg Leu Ser His Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp |     |
|    | 160 165 170   |     |
| 35 | gcc acg gtc gat cag caa aat ggt tat cgc ttc gtg tac agc ctg ccg | 697 |
|    | Ala Thr Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Ser Leu Pro |     |
|    | 175 180 185 190   |     |
| 40 | ctc tcg ccg acc aga ttg tta att gaa gac acg cac tat att gat aat | 745 |
|    | Leu Ser Pro Thr Arg Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Asn |     |
|    | 195 200 205   |     |
| 45 | gcg aca tta gat cct gaa tgc gcg cgg caa aat att tgc gac tat gcc | 793 |
|    | Ala Thr Leu Asp Pro Glu Cys Ala Arg Gln Asn Ile Cys Asp Tyr Ala |     |
|    | 210 215 220   |     |
| 50 | gcg caa cag ggt tgg cag ctt cag aca ctg ctg cga gaa gaa cag ggc | 841 |
|    | Ala Gln Gln Gly Trp Gln Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly |     |
|    | 225 230 235   |     |
| 55 | gcc tta ccc att act ctg tcg ggc aat gcc gac gca ttc tgg cag cag | 889 |
|    | Ala Leu Pro Ile Thr Leu Ser Gly Asn Ala Asp Ala Phe Trp Gln Gln |     |
|    | 240 245 250   |     |
| 60 | cgc ccc ctg gcc tgt agt gga tta cgt gcc ggt ctg ttc cat cct acc | 937 |
|    | Arg Pro Leu Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr |     |
|    | 255 260 265 270   |     |

|    |   |      |
|----|---|------|
|    | acc ggc bat tca ctg ccg ctg gcg gtt gcc gtg gcc gac cgc ctg agt   | 985  |
|    | Thr Gly Tyr Ser Leu Pro Leu Ala Val Ala Val Ala Asp Arg Leu Ser   |      |
|    | 275 280 285   |      |
| 5  | gca ctt gat gtc ttt acg tcg gcc tca att cac cat gcc att acg cat   | 1033 |
|    | Ala Leu Asp Val Phe Thr Ser Ala Ser Ile His His Ala Ile Thr His   |      |
|    | 290 295 300   |      |
| 10 | ttt gcc cgc gag cgc tgg cag cag cag gcc ttt ttc cgc atg ctg aat   | 1081 |
|    | Phe Ala Arg Glu Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn   |      |
|    | 305 310 315   |      |
| 15 | cgc atg ctg ttt tta gcc gga ccc gcc gat tca cgc tgg cgg gtt atg   | 1129 |
|    | Arg Met Leu Phe Leu Ala Gly Pro Ala Asp Ser Arg Trp Arg Val Met   |      |
|    | 320 325 330   |      |
| 20 | cag cgt ttt tat ggt tta cct gaa gat tta att gcc cgt ttt tat gcg   | 1177 |
|    | Gln Arg Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala   |      |
|    | 335 340 345 350   |      |
| 25 | gga aaa ctc acg ctg acc gat cgg cta cgt att ctg agc ggc aag ccg   | 1225 |
|    | Gly Lys Leu Thr Leu Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro   |      |
|    | 355 360 365   |      |
| 30 | cct gtt ccg gta tta gca gca ttg caa gcc att atg acg act           | 1267 |
|    | Pro Val Pro Val Leu Ala Ala Leu Gln Ala Ile Met Thr Thr           |      |
|    | 370 375 380   |      |
| 35 | catcgtaaag gagcgactac atg aaa cca act acg gta att ggt gca ggc ttc | 1320 |
|    | Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe                       |      |
|    | 385 390   |      |
| 40 | ggt gcc ctg gca ctg gca att cgt cta caa gct gcg ggg atc ccc gtc   | 1368 |
|    | Gly Gly Leu Ala Leu Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val   |      |
|    | 395 400 405   |      |
| 45 | tta ctg ctt gaa caa cgt gat aaa ccc gcc ggt cgg gct tat gtc tac   | 1416 |
|    | Leu Leu Leu Glu Gln Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr   |      |
|    | 410 415 420   |      |
| 50 | gag gat cag ggg ttt acc ttt gat gca ggc ccg acg gtt atc acc gat   | 1464 |
|    | Glu Asp Gln Gly Phe Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp   |      |
|    | 425 430 435   |      |
| 55 | ccc agt gcc att gaa gaa ctg ttt gca ctg gca gga aaa cag tta aaa   | 1512 |
|    | Pro Ser Ala Ile Glu Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys   |      |
|    | 440 445 450 455   |      |
| 60 | gag tat gtc gaa ctg ctg ccg gtt acg ccg ttt tac cgc ctg tgt tgg   | 1560 |
|    | Glu Tyr Val Glu Leu Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp   |      |
|    | 460 465 470   |      |

|    |   |      |
|----|---|------|
|    | gag tca ggg aag gtc ttt aat tac gat aac gat caa acc cgg ctc gaa | 1608 |
|    | Glu Ser Gly Lys Val Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu |      |
|    | 475 480 485   |      |
| 5  | gcg cag att cag cag ttt aat ccc cgc gat gtc gaa ggt tat cgt cag | 1656 |
|    | Ala Gln Ile Gln Gln Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln |      |
|    | 490 495 500   |      |
| 10 | ttt ctg gac tat tca cgc gcg gtg ttt aaa gaa ggc tat cta aag ctc | 1704 |
|    | Phe Leu Asp Tyr Ser Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu |      |
|    | 505 510 515   |      |
| 15 | ggt act gtc cct ttt tta tcg ttc aga gac atg ctt cgc gcc gca cct | 1752 |
|    | Gly Thr Val Pro Phe Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro |      |
|    | 520 525 530 535   |      |
| 20 | caa ctg gcg aaa ctg cag gca tgg aga agc gtt tac agt aag gtt gcc | 1800 |
|    | Gln Leu Ala Lys Leu Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala |      |
|    | 540 545 550   |      |
|    | agt tac atc gaa gat gaa cat ctg cgc cag gcg ttt tct ttc cac tcg | 1848 |
|    | Ser Tyr Ile Glu Asp Glu His Leu Arg Gln Ala Phe Ser Phe His Ser |      |
|    | 555 560 565   |      |
| 25 | ctg ttg gtg ggc gcc aat ccc ttc gcc acc tca tcc att tat acg ttg | 1896 |
|    | Leu Leu Val Gly Gly Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu |      |
|    | 570 575 580   |      |
| 30 | ata cac gcg ctg gag cgt gag tgg ggc gtc tgg ttt ccg cgt ggc ggc | 1944 |
|    | Ile His Ala Leu Glu Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly |      |
|    | 585 590 595   |      |
| 35 | acc ggc gca tta gtt cag ggg atg ata aag ctg ttt cag gat ctg ggt | 1992 |
|    | Thr Gly Ala Leu Val Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly |      |
|    | 600 605 610 615   |      |
| 40 | ggc gaa gtc gtg tta aac gcc aga gtc agc cat atg gaa acg aca gga | 2040 |
|    | Gly Glu Val Val Leu Asn Ala Arg Val Ser His Met Glu Thr Thr Gly |      |
|    | 620 625 630   |      |
|    | aac aag att gaa gcc gtg cat tta gag gac ggt cgc agg ttc ctg acg | 2088 |
|    | Asn Lys Ile Glu Ala Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr |      |
|    | 635 640 645   |      |
| 45 | caa gcc gtc gcg tca aat gca gat gtg gtt cat acc tat cgc gac ctg | 2136 |
|    | Gln Ala Val Ala Ser Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu |      |
|    | 650 655 660   |      |
| 50 | tta agc cag cac cct gcc gcg gtt aag cag tcc aac aaa ctg cag act | 2184 |
|    | Leu Ser Gln His Pro Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr |      |
|    | 665 670 675   |      |



|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|--|------|
|    | aa  | g   | c   | g   | c   | a   | t   | g   | a   | g   | a   | a   | c   | t   | c   | t   | t  | g | t | g | c | t | c | t | a | t | t | t | g | g | t | t | t | a | a | t | c | a | c |  | 2232 |
|    | Lys | Arg | Met | Ser | Asn | Ser | Leu | Phe | Val | Leu | Tyr | Phe | Gly | Leu | Asn | His |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|    | 680 |     |     |     |     | 685 |     |     |     |     | 690 |     |     |     |     | 695 |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
| 5  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|    | cat | cat | gat | cag | ctc | gcg | cat | cac | acg | gtt | tgt | ttc | ggc | ccg | cgt | tac |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  | 2280 |
|    | His | His | Asp | Gln | Leu | Ala | His | His | Thr | Val | Cys | Phe | Gly | Pro | Arg | Tyr |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|    |     |     |     |     | 700 |     |     |     |     | 705 |     |     |     |     |     | 710 |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
| 10 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|    | cgc | gag | ctg | att | gac | gaa | att | ttt | aat | cat | gat | ggc | ctc | gca | gag | gac |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  | 2328 |
|    | Arg | Glu | Leu | Ile | Asp | Glu | Ile | Phe | Asn | His | Asp | Gly | Leu | Ala | Glu | Asp |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|    |     |     |     | 715 |     |     |     |     | 720 |     |     |     |     | 725 |     |     |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
| 15 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|    | ttc | tca | ctt | tat | ctg | cac | gcg | ccc | tgt | gtc | acg | gat | tcg | tca | ctg | gcg |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  | 2376 |
|    | Phe | Ser | Leu | Tyr | Leu | His | Ala | Pro | Cys | Val | Thr | Asp | Ser | Ser | Leu | Ala |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|    |     |     | 730 |     |     |     |     | 735 |     |     |     |     | 740 |     |     |     |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
| 20 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|    | cct | gaa | ggc | tgc | ggc | agt | tac | tat | gtg | ttg | gcg | ccg | gtg | ccg | cat | tta |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  | 2424 |
|    | Pro | Glu | Gly | Cys | Gly | Ser | Tyr | Tyr | Val | Leu | Ala | Pro | Val | Pro | His | Leu |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|    |     | 745 |     |     |     |     | 750 |     |     |     |     | 755 |     |     |     |     |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
| 25 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |
|    | ggc | acc | gcg | aac | ctc | gac | tgg | acg | gtt | gag | ggg | cca | aaa | cta | cgc | gac | </ |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  |      |

|    |   |      |
|----|---|------|
|    | tcg aaa agt ttt gcg aca gcc tca aag tta ttt gat gca aaa acc cgg | 2861 |
|    | Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr Arg |      |
|    | 880 885 890   |      |
| 5  | cgc agc gta ctg atg ctc tac gcc tgg tgc cgc cat tgt gac gat gtt | 2909 |
|    | Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp Val |      |
|    | 895 900 905   |      |
| 10 | att gac gat cag acg ctg ggc ttt cag gcc cgg cag cct gcc tta caa | 2957 |
|    | Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu Gln |      |
|    | 910 915 920   |      |
|    | acg ccc gaa caa cgt ctg atg caa ctt gag atg aaa acg cgc cag gcc | 3005 |
| 15 | Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln Ala |      |
|    | 925 930 935 940   |      |
|    | tat gca gga tcg cag atg cac gaa ccg gcg ttt gcg gct ttt cag gaa | 3053 |
| 20 | Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln Glu |      |
|    | 945 950 955   |      |
|    | gtg gct atg gct cat gat atc gcc ccg gct tac gcg ttt gat cat ctg | 3101 |
|    | Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His Leu |      |
|    | 960 965 970   |      |
| 25 | gaa ggc ttc gcc atg gat gta cgc gaa gcg caa tac agc caa ctg gat | 3149 |
|    | Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu Asp |      |
|    | 975 980 985   |      |
| 30 | gat acg ctg cgc tat tgc tat cac gtt gca gcc gtt gtc gcc ttg atg | 3197 |
|    | Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu Met |      |
|    | 990 995 1000  |      |
|    | atg gcg caa atc atg ggc gtg cgg gat aac gcc acg ctg gac cgc     | 3242 |
| 35 | Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg     |      |
|    | 1005 1010 1015  |      |
|    | gcc tgt gac ctt ggg ctg gca ttt cag ttg acc aat att gct cgc     | 3287 |
| 40 | Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg     |      |
|    | 1020 1025 1030  |      |
|    | gat att gtg gac gat gcg cat gcg ggc cgc tgt tat ctg ccg gca     | 3332 |
|    | Asp Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala     |      |
|    | 1035 1040 1045  |      |
| 45 | agc tgg ctg gag cat gaa ggt ctg aac aaa gag aat tat gcg gca     | 3377 |
|    | Ser Trp Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala     |      |
|    | 1050 1055 1060  |      |
| 50 | cct gaa aac cgt cag gcg ctg agc cgt atc gcc cgt cgt ttg gtg     | 3422 |
|    | Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val     |      |
|    | 1065 1070 1075  |      |

|    |   |       |
|----|---|-------|
| 5  | 'cag gaa gca gaa cct tac tat ttg tct gcc aca gcc ggc ctg gca<br>Gln Glu Ala Glu Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala<br>1080 1085 1090   | 3467* |
|    | 'ggg ttg ccc ctg cgt tcc gcc tgg gca atc gct acg gcg aag cag<br>Gly Leu Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln<br>1095 1100 1105   | 3512  |
|    | 10 gtt tac cgg aaa ata ggt gtc aaa gtt gaa cag gcc ggt cag caa<br>Val Tyr Arg Lys Ile Gly Val Lys Val Glu Gln Ala Gly Gln Gln<br>1110 1115 1120 | 3557  |
|    | 15 gcc tgg gat cag cgg cag tca acg acc acg ccc gaa aaa tta acg<br>Ala Trp Asp Gln Arg Gln Ser Thr Thr Thr Pro Glu Lys Leu Thr<br>1125 1130 1135 | 3602  |
|    | 20 ctg ctg ctg gcc gcc tct ggt cag gcc ctt act tcc cgg atg cgg<br>Leu Leu Leu Ala Ala Ser Gly Gln Ala Leu Thr Ser Arg Met Arg<br>1140 1145 1150 | 3647  |
| 25 | gct cat cct ccc cgc cct gcg cat ctc tgg cag cgc ccg ctc<br>Ala His Pro Pro Arg Pro Ala His Leu Trp Gln Arg Pro Leu<br>1155 1160 1165            | 3689  |
|    | tagcgccatg tctttcccg agcgtcgccct gaagttttga caggggcggc gcatagagga   | 3749  |
|    | agccaaaaga aacacaacct tctttgcccc tgacggcggtg atgcatacgg tgcgccatat  | 3809  |
|    | 30 acaaccgttt gaggtagccc ttgcgtggaa tatagcggaa tggccaacgt tgatgcacca  | 3869  |
|    | gcccgtcgtg caccataaaa tagagtaatc catacgccgt catacctgcg ccaatccact   | 3929  |
| 35 | ggagcggcca cattcctgta ctgccagat aatcagcag gatcgataat gcagcaaaaa   | 3989  |
|    | ccacggcata aagatcgta acttcaaacy cacctttacg cggttcatga tgtgaaagat  | 4049  |
|    | gccatcccca accccagccg tgcgatgatgt atttgtgtgc cagtgcagca atcacttcca  | 4109  |
|    | 40 tgccaatcac ggtaacgaaa acgatcaggg cattccaaat ccacaacata atttctccg   | 4169  |
|    | tagagacgtc tggcagcagg cttaaggatt caattttaac agagattagc cgatctggcg   | 4229  |
| 45 | gcgggaaggg aaaaaggcgc gccagaaagg cgcgccaggg atcagaagtc ggctttcaga   | 4289  |
|    | accacacggt agttggcttt acctgcacga acatggtcca gtgcatcggt gattttcgac   | 4349  |
|    | atcgggaagt actccactgt cggcgcaata tctgtacggc cagccagctt cagcagtgaa   | 4409  |
|    | 50 cgcagctgcg caggtgaacc gggtgaagaa cccgtcacgg cgcggtcgcc taaaatcagg  | 4469  |
|    | ctgaaagccg ggcacgtcaa acggcttcag tacggcaccc acggtatgga acttaccgcg   | 4529  |

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<213> Erwinia uredovora

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Leu Leu Ile Asp Ala Ala Pro Gln Ala Gly Gly Asn His Thr Trp Ser  
35 40 45

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Phe His His Asp Asp Leu Thr Glu Ser Gln His Arg Trp Ile Ala Pro  
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Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Thr Arg  
65 70 75 80

40

Arg Arg Lys Leu Asn Ser Gly Tyr Phe Cys Ile Thr Ser Gln Arg Phe  
85 90 95

45

Ala Glu Val Leu Gln Arg Gln Phe Gly Pro His Leu Trp Met Asp Thr  
100 105 110

Ala Val Ala Glu Val Asn Ala Glu Ser Val Arg Leu Lys Lys Gly Gln  
115 120 125

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Val Ile Gly Ala Arg Ala Val Ile Asp Gly Arg Gly Tyr Ala Ala Asn  
130 135 140

5 Ser Ala Leu Ser Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Arg  
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 195 200 205  
 20 Leu Asp Pro Glu Cys Ala Arg Gln Asn Ile Cys Asp Tyr Ala Ala Gln  
 210 215 220  
 25 Gln Gly Trp Gln Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu  
 225 230 235 240  
 Pro Ile Thr Leu Ser Gly Asn Ala Asp Ala Phe Trp Gln Gln Arg Pro  
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 260 265 270  
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 275 280 285  
 40 Asp Val Phe Thr Ser Ala Ser Ile His His Ala Ile Thr His Phe Ala  
 290 295 300  
 45 Arg Glu Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met  
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 Leu Phe Leu Ala Gly Pro Ala Asp Ser Arg Trp Arg Val Met Gln Arg  
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35 Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe  
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40 Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu  
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45 Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu  
 65 70 75 80

50 Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val  
 85 90 95

Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln  
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Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser  
 115 120 125

Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe  
 130 135 140  
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 Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu  
 145 150 155 160  
 10  
 Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp  
 165 170 175  
 15  
 Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly  
 180 185 190  
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 Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu  
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 Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu  
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 Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser  
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 275 280 285  
 Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn  
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 Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu  
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 Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp  
 325 330 335

5  
10  
15  
20  
25  
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40  
45  
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Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu  
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His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly  
355 360 365

Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu  
370 375 380

Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr  
385 390 395 400

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His  
405 410 415

Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His  
420 425 430

Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe  
435 440 445

Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly  
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Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala  
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 Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln  
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 Pro Ala Leu Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys  
 50 55 60  
 20  
 Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala  
 65 70 75 80  
 25  
 Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala  
 85 90 95  
 30  
 Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr  
 100 105 110  
 35  
 Ser Gln Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val  
 115 120 125  
 40  
 Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr  
 130 135 140  
 45  
 Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile  
 145 150 155 160  
 50  
 Ala Arg Asp Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro  
 165 170 175  
 Ala Ser Trp Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala  
 180 185 190  
 Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln  
 195 200 205



<211> 32  
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20 tttttgtcga cacgttatgc tcacaacccc gg 32

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25 <211> 679  
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45 ctcgagcgat aaacgctcac ttggttaatc atttcactct tcaattatct ataatgatga 60  
gtgatcagaa ttacatgtga gaaatt atg caa acg gaa cac gtc att tta ttg 113  
Met Gln Thr Glu His Val Ile Leu Leu  
1 5

50 aat gca cag gga gtt ccc acg ggt acg ctg gaa aag tat gcc gca cac 161  
Asn Ala Gln Gly Val Pro Thr Gly Thr Leu Glu Lys Tyr Ala Ala His  
10 15 20 25

|    |   |     |
|----|---|-----|
|    | acg gca gac acc cgc tta cat ctc gcg ttc tcc agt tgg ctg ttt aat | 209 |
|    | Thr Ala Asp Thr Arg Leu His Leu Ala Phe Ser Ser Trp Leu Phe Asn |     |
|    | 30 35 40  |     |
| 5  | gcc aaa gga caa tta tta gtt acc cgc cgc gca ctg agc aaa aaa gca | 257 |
|    | Ala Lys Gly Gln Leu Leu Val Thr Arg Arg Ala Leu Ser Lys Lys Ala |     |
|    | 45 50 55  |     |
| 10 | tgg cct ggc gtg tgg act aac tcg gtt tgt ggg cac cca caa ctg gga | 305 |
|    | Trp Pro Gly Val Trp Thr Asn Ser Val Cys Gly His Pro Gln Leu Gly |     |
|    | 60 65 70  |     |
|    | gaa agc aac gaa gac gca gtg atc cgc cgt tgc cgt tat gag ctt ggc | 353 |
| 15 | Glu Ser Asn Glu Asp Ala Val Ile Arg Arg Cys Arg Tyr Glu Leu Gly |     |
|    | 75 80 85  |     |
|    | gtg gaa att acg cct cct gaa tct atc tat cct gac ttt cgc tac cgc | 401 |
|    | Val Glu Ile Thr Pro Pro Glu Ser Ile Tyr Pro Asp Phe Arg Tyr Arg |     |
| 20 | 90 95 100 105   |     |
|    | gcc acc gat ccg agt ggc att gtg gaa aat gaa gtg tgt ccg gta ttt | 449 |
|    | Ala Thr Asp Pro Ser Gly Ile Val Glu Asn Glu Val Cys Pro Val Phe |     |
|    | 110 115 120   |     |
| 25 | gcc gca cgc acc act agt gcg tta cag atc aat gat gat gaa gtg atg | 497 |
|    | Ala Ala Arg Thr Thr Ser Ala Leu Gln Ile Asn Asp Asp Glu Val Met |     |
|    | 125 130 135   |     |
| 30 | gat tat caa tgg tgt gat tta gca gat gta tta cac ggt att gat gcc | 545 |
|    | Asp Tyr Gln Trp Cys Asp Leu Ala Asp Val Leu His Gly Ile Asp Ala |     |
|    | 140 145 150   |     |
|    | acg ccg tgg gcg ttc agt ccg tgg atg gtg atg cag gcg aca aat cgc | 593 |
| 35 | Thr Pro Trp Ala Phe Ser Pro Trp Met Val Met Gln Ala Thr Asn Arg |     |
|    | 155 160 165   |     |
|    | gaa gcc aga aaa cga tta tct gca ttt acc cag ctt aaa taa         | 635 |
|    | Glu Ala Arg Lys Arg Leu Ser Ala Phe Thr Gln Leu Lys             |     |
| 40 | 170 175 180   |     |
|    | aaaaaccccg acatttgcg gggttgtgag cataacgtgt cgac                 | 679 |
| 45 | <210> 31  |     |
|    | <211> 182   |     |
|    | <212> PRT   |     |
| 50 | <213> Escherichia coli  |     |

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5 Met Gln Thr Glu His Val Ile Leu Leu Asn Ala Gln Gly Val Pro Thr  
 1 5 10 15

10 Gly Thr Leu Glu Lys Tyr Ala Ala His Thr Ala Asp Thr Arg Leu His  
 20 25 30

15 Leu Ala Phe Ser Ser Trp Leu Phe Asn Ala Lys Gly Gln Leu Leu Val  
 35 40 45

20 Thr Arg Arg Ala Leu Ser Lys Lys Ala Trp Pro Gly Val Trp Thr Asn  
 50 55 60

25 Ser Val Cys Gly His Pro Gln Leu Gly Glu Ser Asn Glu Asp Ala Val  
 65 70 75 80

30 Ile Arg Arg Cys Arg Tyr Glu Leu Gly Val Glu Ile Thr Pro Pro Glu  
 85 90 95

35 Ser Ile Tyr Pro Asp Phe Arg Tyr Arg Ala Thr Asp Pro Ser Gly Ile  
 100 105 110

40 Val Glu Asn Glu Val Cys Pro Val Phe Ala Ala Arg Thr Thr Ser Ala  
 115 120 125

45 Leu Gln Ile Asn Asp Asp Glu Val Met Asp Tyr Gln Trp Cys Asp Leu  
 130 135 140

50 Ala Asp Val Leu His Gly Ile Asp Ala Thr Pro Trp Ala Phe Ser Pro  
 145 150 155 160

45 Trp Met Val Met Gln Ala Thr Asn Arg Glu Ala Arg Lys Arg Leu Ser  
 165 170 175

50 Ala Phe Thr Gln Leu Lys  
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<210> 32  
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tttttaagct ttcacttttt tcttgtaacc aa  
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<210> 34  
<211> 962

31

32

&lt;212&gt; DNA

&lt;213&gt; Archaeoglobus fulgidus

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&lt;220&gt;

&lt;221&gt; CDS

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&lt;222&gt; (3) .. (956)

&lt;223&gt;

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&lt;400&gt; 34

cc atg gtg aag gag gaa ata gcg aaa agg gcc gaa ata atc aac aaa 47

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Met Val Lys Glu Glu Ile Ala Lys Arg Ala Glu Ile Ile Asn Lys

1

5

10

15

gcc att gaa gag ctt ctg ccc gaa agg gag ccg att gga ctc tac aaa 95

Ala Ile Glu Glu Leu Leu Pro Glu Arg Glu Pro Ile Gly Leu Tyr Lys

20

25

30

25

gcc gca agg cat ctg atc aaa gca ggt ggc aag agg cta agg cct gta 143

Ala Ala Arg His Leu Ile Lys Ala Gly Gly Lys Arg Leu Arg Pro Val

35

40

45

30

ata agc ctc tta gca gtc gaa gcc ctt ggg aaa gac tac aga aag att 191

Ile Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile

50

55

60

35

atc ccg gct gct gtc agc att gaa aca atc cac aac ttc acc ctc gtg 239

Ile Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val

65

70

75

40

cat gac gac ata atg gac agg gac gag atg agg agg gga gtt ccg acg 287

His Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr

80

85

90

95

45

gta cac agg gtt tat ggg gaa gcg acg gcc att tta gca ggc gac aca 335

Val His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr

100

105

110

50

ctc ttt gct gaa gcc ttc aag ctg ctg aca aag tgc gat gtt gag agc 383

Leu Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser

115

120

125

50

gag gga atc aga aaa gct aca gaa atg ctt tcg gac gtt tgc ata aaa 431

Glu Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys

130

135

140

ata tgc gag ggg cag tac tac gac atg agc ttt gag aaa aag gag agc 479  
 Ile Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser  
 145 150 155  
 5 gtt tcc gag gag gag tat ctc agg atg gtc gag ctg aag acc gga gtg 527  
 Val Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val  
 160 165 170 175  
 10 ctg att gca gct tct gca gca tta cct gcg gtg ctt ttt ggg gag agc 575  
 Leu Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser  
 180 185 190  
 15 gag gaa att gta aag gcg ctg tgg gac tac gga gtt ctt agc ggt att 623  
 Glu Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile  
 195 200 205  
 20 ggc ttc cag atc cag gac gac ctg ctt gac ctg act gag gag acc gga 671  
 Gly Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly  
 210 215 220  
 25 aag gac tgg gga agc gac ctg ctt aaa ggg aag aaa acc ctg att gtc 719  
 Lys Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val  
 225 230 235  
 30 ata aag gcg ttc gaa aag gga gtg aag cta aag acg ttt gga aag gaa 767  
 Ile Lys Ala Phe Glu Lys Gly Val Lys Leu Lys Thr Phe Gly Lys Glu  
 240 245 250 255  
 35 aag gcg gac gtc tct gag att aga gat gat atc gaa aag tta aga gag 815  
 Lys Ala Asp Val Ser Glu Ile Arg Asp Asp Ile Glu Lys Leu Arg Glu  
 260 265 270  
 40 tgt ggt gcg att gat tac gct gcc agc atg gca aga aag atg gct gaa 863  
 Cys Gly Ala Ile Asp Tyr Ala Ala Ser Met Ala Arg Lys Met Ala Glu  
 275 280 285  
 45 gag gcg aaa aga aag ctc gaa gtt ctg cct gaa agc aaa gcc aag gaa 911  
 Glu Ala Lys Arg Lys Leu Glu Val Leu Pro Glu Ser Lys Ala Lys Glu  
 290 295 300  
 50 aca ctg ctg gaa ctt acc gac ttc ttg gtt aca aga aaa aag tga 956  
 Thr Leu Leu Glu Leu Thr Asp Phe Leu Val Thr Arg Lys Lys  
 305 310 315  
 55 aagctt 962  
 <210> 35  
 <211> 317



&lt;212&gt; PRT

&lt;213&gt; Archaeoglobus fulgidus

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&lt;400&gt; 35

10 Met Val Lys Glu Glu Ile Ala Lys Arg Ala Glu Ile Ile Asn Lys Ala  
1 5 10 15

15 Ile Glu Glu Leu Leu Pro Glu Arg Glu Pro Ile Gly Leu Tyr Lys Ala  
20 25 30

Ala Arg His Leu Ile Lys Ala Gly Gly Lys Arg Leu Arg Pro Val Ile  
35 40 45

20 Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile Ile  
50 55 60

25 Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val His  
65 70 75 80

30 Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr Val  
85 90 95

35 His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr Leu  
100 105 110

Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser Glu  
115 120 125

40 Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys Ile  
130 135 140

45 Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser Val  
145 150 155 160

50 Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val Leu  
165 170 175

Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser Glu  
 180 185 190

5 Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile Gly  
 195 200 205

10 Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly Lys  
 210 215 220

15 Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val Ile  
 225 230 235 240

Lys Ala Phe Glu Lys Gly Val Lys Leu Lys Thr Phe Gly Lys Glu Lys  
 245 250 255

20 Ala Asp Val Ser Glu Ile Arg Asp Asp Ile Glu Lys Leu Arg Glu Cys  
 260 265 270

25 Gly Ala Ile Asp Tyr Ala Ala Ser Met Ala Arg Lys Met Ala Glu Glu  
 275 280 285

30 Ala Lys Arg Lys Leu Glu Val Leu Pro Glu Ser Lys Ala Lys Glu Thr  
 290 295 300

35 Leu Leu Glu Leu Thr Asp Phe Leu Val Thr Arg Lys Lys  
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<210> 36

40 <211> 1293

<212> DNA

<213> Archaeoglobus fulgidus

45 <220>

<221> CDS

50 <222> (206)..(1159)

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 gccccccctc gacgccgtcg ttcaatgaga atggataaga ggctcgtggg attgacgtga 120  
 10 gggggcaggg atggctatat ttctgggagc gaactccggg cgaggatcta gttgtaggga 180  
 gggattcatg acaccacaaa cagcc atg gtg aag gag gaa ata gcg aaa agg 232  
 Met Val Lys Glu Glu Ile Ala Lys Arg  
 1 5  
 15 gcc gaa ata atc aac aaa gcc att gaa gag ctt ctg ccc gaa agg gag 280  
 Ala Glu Ile Ile Asn Lys Ala Ile Glu Glu Leu Leu Pro Glu Arg Glu  
 10 15 20 25  
 20 ccg att gga ctc tac aaa gcc gca agg cat ctg atc aaa gca ggt gcc 328  
 Pro Ile Gly Leu Tyr Lys Ala Ala Arg His Leu Ile Lys Ala Gly Gly  
 30 35 40  
 aag agg cta agg cct gta ata agc ctc tta gca gtc gaa gcc ctt ggg 376  
 25 Lys Arg Leu Arg Pro Val Ile Ser Leu Leu Ala Val Glu Ala Leu Gly  
 45 50 55  
 aaa gac tac aga aag att atc ccg gct gct gtc agc att gaa aca atc 424  
 30 Lys Asp Tyr Arg Lys Ile Ile Pro Ala Ala Val Ser Ile Glu Thr Ile  
 60 65 70  
 cac aac ttc acc ctc gfg cat gac gac ata atg gac agg gac gag atg 472  
 His Asn Phe Thr Leu Val His Asp Asp Ile Met Asp Arg Asp Glu Met  
 75 80 85  
 35 agg agg gga gtt ccg acg gta cac agg gtt tat ggg gaa gcg acg gcc 520  
 Arg Arg Gly Val Pro Thr Val His Arg Val Tyr Gly Glu Ala Thr Ala  
 90 95 100 105  
 40 att tta gca ggc gac aca ctc ttt gct gaa gcc ttc aag ctg ctg aca 568  
 Ile Leu Ala Gly Asp Thr Leu Phe Ala Glu Ala Phe Lys Leu Leu Thr  
 110 115 120  
 aag tgc gat gtt gag agc gag gga atc aga aaa gct aca gaa atg ctt 616  
 45 Lys Cys Asp Val Glu Ser Glu Gly Ile Arg Lys Ala Thr Glu Met Leu  
 125 130 135  
 tcg gac gtt tgc ata aaa ata tgc gag ggg cag tac tac gac atg agc 664  
 Ser Asp Val Cys Ile Lys Ile Cys Glu Gly Gln Tyr Tyr Asp Met Ser  
 50 140 145 150  
 ttt gag aaa aag gag agc gtt tcc gag gag gag tat ctc agg atg gtc 712

## 60

|    |  |      |
|----|--|------|
|    | Phe Glu Lys Lys Glu Ser Val Ser Glu Glu Glu Tyr Leu Arg Met Val  |      |
|    | 155 160 165  |      |
| 5  | gag ctg aag acc gga gtg ctg att gca gct tct gca gca tta cct gcg<br>Glu Leu Lys Thr Gly Val Leu Ile Ala Ala Ser Ala Ala Leu Pro Ala | 760  |
|    | 170 175 180 185  |      |
| 10 | gtg ctt ttt ggg gag agc gag gaa att gta aag gcg ctg tgg gac tac<br>Val Leu Phe Gly Glu Ser Glu Glu Ile Val Lys Ala Leu Trp Asp Tyr | 808  |
|    | 190 195 200  |      |
| 15 | gga gtt ctt agc ggt att ggc ttc cag atc cag gac gac ctg ctt gac<br>Gly Val Leu Ser Gly Ile Gly Phe Gln Ile Gln Asp Asp Leu Leu Asp | 856  |
|    | 205 210 215  |      |
| 20 | ctg act gag gag acc gga aag gac tgg gga agc gac ctg ctt aaa ggg<br>Leu Thr Glu Glu Thr Gly Lys Asp Trp Gly Ser Asp Leu Leu Lys Gly | 904  |
|    | 220 225 230  |      |
| 25 | aag aaa acc ctg att gtc ata aag gcg ttc gaa aag gga gtg aag cta<br>Lys Lys Thr Leu Ile Val Ile Lys Ala Phe Glu Lys Gly Val Lys Leu | 952  |
|    | 235 240 245  |      |
| 30 | aag acg ttt gga aag gaa aag gcg gac gtc tct gag att aga gat gat<br>Lys Thr Phe Gly Lys Glu Lys Ala Asp Val Ser Glu Ile Arg Asp Asp | 1000 |
|    | 250 255 260 265  |      |
| 35 | atc gaa aag tta aga gag tgt ggt gcg att gat tac gct gcc agc atg<br>Ile Glu Lys Leu Arg Glu Cys Gly Ala Ile Asp Tyr Ala Ala Ser Met | 1048 |
|    | 270 275 280  |      |
| 40 | gca aga aag atg gct gaa gag gcg aag aga aag ctc gaa gtt ctg cct<br>Ala Arg Lys Met Ala Glu Glu Ala Lys Arg Lys Leu Glu Val Leu Pro | 1096 |
|    | 285 290 295  |      |
| 45 | gaa agc aaa gcc aag gaa aca ctg ctg gaa ctt acc gac ttc ttg gtt<br>Glu Ser Lys Ala Lys Glu Thr Leu Leu Glu Leu Thr Asp Phe Leu Val | 1144 |
|    | 300 305 310  |      |
| 50 | aca aga aaa aag tga aagcttcaat tgcattgctct agatgatcaa agaattcctg<br>Thr Arg Lys Lys  | 1199 |
|    | 315  |      |
| 55 | gcctagtcta taggaggttt tgaaaagaaa ggagcaataa tcattttctt gttctatcaa  | 1259 |
| 60 | gaggggtgcta ttgctccttt ctttttttct cgag   | 1293 |
|    | <210> 37   |      |
|    | <211> 317  |      |

&lt;212&gt; PRT

&lt;213&gt; Archaeoglobus fulgidus

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&lt;400&gt; 37

10 Met Val Lys Glu Glu Ile Ala Lys Arg Ala Glu Ile Ile Asn Lys Ala  
1 5 10 15

15 Ile Glu Glu Leu Leu Pro Glu Arg Glu Pro Ile Gly Leu Tyr Lys Ala  
20 25 30

20 Ala Arg His Leu Ile Lys Ala Gly Gly Lys Arg Leu Arg Pro Val Ile  
35 40 45

Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile Ile  
50 55 60

25 Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val His  
65 70 75 80

30 Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr Val  
85 90 95

35 His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr Leu  
100 105 110

Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser Glu  
115 120 125

40 Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys Ile  
130 135 140

45 Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser Val  
145 150 155 160

50 Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val Leu  
165 170 175

## 62

Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser Glu  
 180 185 190

5 Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile Gly  
 195 200 205

10 Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly Lys  
 210 215 220

15 Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val Ile  
 225 230 235 240

Lys Ala Phe Glu Lys Gly Val Lys Leu Lys Thr Phe Gly Lys Glu Lys  
 245 250 255

20 Ala Asp Val Ser Glu Ile Arg Asp Asp Ile Glu Lys Leu Arg Glu Cys  
 260 265 270

25 Gly Ala Ile Asp Tyr Ala Ala Ser Met Ala Arg Lys Met Ala Glu Glu  
 275 280 285

30 Ala Lys Arg Lys Leu Glu Val Leu Pro Glu Ser Lys Ala Lys Glu Thr  
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35 Leu Leu Glu Leu Thr Asp Phe Leu Val Thr Arg Lys Lys  
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<210> 38

<211> 35

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<213> Artificial sequence

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&lt;210&gt; 39

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&lt;211&gt; 38

&lt;212&gt; DNA

15 <213> Artificial sequence

&lt;220&gt;

20

&lt;221&gt; Primer

&lt;222&gt; (1)..(38)

25 <223>

&lt;400&gt; 39

30 aagcttggtt gatcagaaga agaagaagaa gatgaact

38

&lt;210&gt; 40

35 <211> 647

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

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&lt;220&gt;

45 <221> Promoter

&lt;222&gt; (1)..(647)

&lt;223&gt;

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 taatacttta cccgtgtaaa tcaaaaacaa aaaggctttt gagctttttg tagttgaatt 120  
 5 tctctggctg atcttttctg tacagattca tatactctga gagacgatat cattgattat 180  
 ttgagcttct tttgaactat ttcgtgtaat ttgggatgag agctctatgt atgtgtgtaa 240  
 10 actttgaaga caacaagaaa ggtaacaagt gagggaggga tgactccatg tcaaaataga 300  
 tgtcataaga ggcccatcaa taagtgttg agccpattag ctagcccagt aactaccaga 360  
 ttgtgagatg gatgtgtgaa cagttttttt ttgatgtag gactgaaatg tgaacaacag 420  
 15 gcgcatgaaa ggctaaatta ggacaatgat aagcagaaat aactatcct ctctaact 480  
 tggcctcaca ttgcccttca cacaatccac acacatccaa tcacaacctc atcatatc 540  
 20 tcccgctaata ctttttttct ttgatctttt tttttttgt tattattttt ttgactttga 600  
 tctcccatca gttcatcttc ttcttcttct tctgatcaac caagctt 647  
 25 <210> 41  
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 30 <213> Artificial sequence  
 35 <220>  
 <221> primer\_bind  
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 40 <223>  
 45 <400> 41  
 gagctcactc actgatttcc attgcttg 28  
 <210> 42  
 50 <211> 23



<212> DNA

<213> Artificial sequence

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<220>

<221> Primer

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<222> (1)..(23)

<223>

15

<400> 42

aagcttttgt tgaagagatt tgg

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<210> 43

<211> 37

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<212> DNA

<213> Artificial sequence

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<220>

<221> primer\_bind

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<210> 44

<211> 34

<212> DNA

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<213> Artificial sequence

<220>

5 <221> primer\_bind

<222> (1)..(34)

<223>

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<210> 45

<211> 777

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<212> DNA

<213> Arabidopsis thaliana

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<222> (1)..(777)

<223>

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40 tagtttcaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactggtcga 120

agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagttagga 180

ccaaacatta tctacaaaca aagacttttc tcctaacttg tgattccttc ttaaacccta 240

45 ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta 300

atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360

50 tatatatctc tttcttctta tttcccaaata taacagacaa aagtagaata ttggctttta 420

acaccaatat aaaaacttgc ttcacaccta aacacttttg tttactttag ggtaagtgca 480

aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540  
 ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600  
 5 tcacttagtt ttcatcaact tctgaactta cctttcatgg attaggcaat actttccatt, 660  
 tttagtaact caagtgagacc ctttacttct tcaactccat ctctctcttt ctatttcact 720  
 10 tctttcttct cattatatct cttgtcctct ccaccaaata tcttcaacaa aaagctt 777

<210> 46  
 15 <211> 804  
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 <213> Synechococcus WM8102  
 20  
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 25 <221> CDS  
 <222> (1)..(804)  
 <223>  
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 cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96  
 40 Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala  
 20 25 30  
 ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc 144  
 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu  
 35 40 45  
 45 tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg 192  
 Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu  
 50 55 60  
 50 ttg att ggc agc ttg att ctg ctc aga gca ttt ctg cac acc ggg ctg 240  
 Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu  
 65 70 75 80

|    |   |     |
|----|---|-----|
|    | ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat | 288 |
|    | Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His |     |
|    | 85 90 95  |     |
| 5  | ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca | 336 |
|    | Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala |     |
|    | 100 105 110   |     |
| 10 | ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac ctg | 384 |
|    | Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu |     |
|    | 115 120 125   |     |
| 15 | gca ccg gag acg ttc cag gat cct gac tac caa cgt tgc acc aat aac | 432 |
|    | Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn |     |
|    | 130 135 140   |     |
| 20 | aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg | 480 |
|    | Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met |     |
|    | 145 150 155 160   |     |
| 25 | cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc | 528 |
|    | Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu |     |
|    | 165 170 175   |     |
| 30 | aac ggt tct gat ctc cct gct cag atc atg cat ctg ctg ttg ttc agc | 576 |
|    | Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser |     |
|    | 180 185 190   |     |
| 35 | gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc | 624 |
|    | Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr |     |
|    | 195 200 205   |     |
| 40 | tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg | 672 |
|    | Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr |     |
|    | 210 215 220   |     |
| 45 | cgc agc ctg gct ttg cat cca gcc ctc tct ttc gca gct tgt tac aac | 720 |
|    | Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn |     |
|    | 225 230 235 240   |     |
| 50 | ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt | 768 |
|    | Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe |     |
|    | 245 250 255   |     |
| 55 | cag ctg cca caa ctt cga aat gaa tca ttc act tga                 | 804 |
|    | Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr                     |     |
|    | 260 265   |     |
| 60 | <210> 47  |     |

&lt;211&gt; 267

&lt;212&gt; PRT

5 &lt;213&gt; Synechococcus WH8102

&lt;400&gt; 47

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Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His  
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Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala  
20 25 30

20

Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu  
35 40 45

25

Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu  
50 55 60

30

Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu  
65 70 75 80

Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His  
85 90 95

35

Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala  
100 105 110

40

Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu  
115 120 125

45

Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn  
130 135 140

Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met  
145 150 155 160

50

Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu  
165 170 175

Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser  
 180 185 190  
 5  
 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr  
 195 200 205  
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 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr  
 210 215 220  
 15  
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn  
 225 230 235 240  
 20  
 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe  
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 260 265  
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 Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His  
 1 5 10 15  
 50  
 cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|    | Gln | Pro | Ser | Cys | Ser | Ser | Trp | Val | Ala | Asn | Glu | Phe | Ser | Pro | Gln | Ala |     |
|    |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| 5  | ctc | aaa | ggg | ttg | gct | ctg | gct | ggg | ctg | att | gga | tca | gcc | ttg | ctg | ctc | 144 |
|    | Leu | Lys | Gly | Leu | Ala | Leu | Ala | Gly | Leu | Ile | Gly | Ser | Ala | Trp | Leu | Leu |     |
|    |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| 10 | tcc | ctg | ggc | ctg | agc | tac | acc | ctg | cca | ctt | gat | cag | acg | cct | ggg | ctg | 192 |
|    | Ser | Leu | Gly | Leu | Ser | Tyr | Thr | Leu | Pro | Leu | Asp | Gln | Thr | Pro | Gly | Leu |     |
|    |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| 15 | ttg | att | ggc | agc | ttg | att | ctg | tgg | cag | acc | ttt | ctg | cac | acc | ggg | ctg | 240 |
|    | Leu | Ile | Gly | Ser | Leu | Ile | Leu | Trp | Gln | Thr | Phe | Leu | His | Thr | Gly | Leu |     |
|    | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| 20 | ttc | atc | gtt | gcc | cac | gat | tcc | atg | cac | gcc | agt | ctg | gtt | ccg | ggg | cat | 288 |
|    | Phe | Ile | Val | Ala | His | Asp | Ser | Met | His | Ala | Ser | Leu | Val | Pro | Gly | His |     |
|    |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| 25 | ccc | gga | ttg | aac | cgc | tgg | atc | ggc | aaa | gtg | tat | ttg | ttg | gtg | tat | gca | 336 |
|    | Pro | Gly | Leu | Asn | Arg | Trp | Ile | Gly | Lys | Val | Tyr | Leu | Leu | Val | Tyr | Ala |     |
|    |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| 30 | ggc | ttg | tct | tat | gag | cgt | tgt | tcc | cgc | aac | cac | aga | cgt | cat | cac | ctg | 384 |
|    | Gly | Leu | Ser | Tyr | Glu | Arg | Cys | Ser | Arg | Asn | His | Arg | Arg | His | His | Leu |     |
|    |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| 35 | gca | ccg | gag | acg | ttc | cag | gat | cct | gac | tac | caa | cgt | tgc | acc | aat | aac | 432 |
|    | Ala | Pro | Glu | Thr | Phe | Gln | Asp | Pro | Asp | Tyr | Gln | Arg | Cys | Thr | Asn | Asn |     |
|    |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| 40 | aac | atc | cta | gat | tgg | tat | gtt | cac | ttc | atg | ggc | aac | tat | ctg | ggc | atg | 480 |
|    | Asn | Ile | Leu | Asp | Trp | Tyr | Val | His | Phe | Met | Gly | Asn | Tyr | Leu | Gly | Met |     |
|    | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |     |
| 45 | cgg | caa | ctg | tta | aat | cta | agc | tgt | ctt | tgg | ctg | gcg | cta | atc | att | ctc | 528 |
|    | Arg | Gln | Leu | Leu | Asn | Leu | Ser | Cys | Leu | Trp | Leu | Ala | Leu | Ile | Ile | Leu |     |
|    |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| 50 | aac | ggg | tct | gat | ctc | cct | gct | cag | atc | atg | cat | ctg | ctg | ttg | ttc | agc | 576 |
|    | Asn | Gly | Ser | Asp | Leu | Pro | Ala | Gln | Ile | Met | His | Leu | Leu | Leu | Phe | Ser |     |
|    |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| 55 | gtt | ctg | ccg | ttg | atc | atc | agt | tcc | tgt | caa | ttg | ttt | cta | gtg | gga | acc | 624 |
|    | Val | Leu | Pro | Leu | Ile | Ile | Ser | Ser | Cys | Gln | Leu | Phe | Leu | Val | Gly | Thr |     |
|    |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| 60 | tgg | tta | ccc | cac | cga | cgt | ggg | gcc | acg | aca | cga | ccg | ggc | gtg | aca | acg | 672 |
|    | Trp | Leu | Pro | His | Arg | Arg | Gly | Ala | Thr | Thr | Arg | Pro | Gly | Val | Thr | Thr |     |
|    |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| 65 | cgc | agc | ctg | gct | ttg | cat | cca | gcc | ctc | tct | ttc | gca | gct | tgt | tac | aac | 720 |





Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu  
 115 120 125

5 Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn  
 130 135 140

10 Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met  
 145 150 155 160

Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu  
 165 170 175

15 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser  
 180 185 190

20 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr  
 195 200 205

25 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr  
 210 215 220

30 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn  
 225 230 235 240

Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe  
 245 250 255

35 Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr  
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Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala  
                20                         25                         30

ctc, aaa ggg ttg gct ctg gct ggt ctg, att gga tca gcc tgg ctg ctc 144  
Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu  
20 35 40 45

tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg 192  
Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu  
50 55 60

ttg att ggc agc ttg att ctg ctc aga gca ttt ctg cac acc ggg ctg 240  
Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu  
65 70 75 80

**30**    ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat                  **288**

Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His

       85                      90                      95

ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca  
35 Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala

100                      105                      110

ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac gga 384  
Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Gly  
40 115 120 125

cat cct ggt act gat tta gat cct gac tac caa cgt tgc acc aat aac 432  
His Pro Gly Thr Asp Leu Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn  
130 135 140

aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg 480  
Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met  
145 150 155 160

50    cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc                      528  
     Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu  
                        165                      170                      175

aac ggt tct gat ctc cct gct cag atc atg cat ctg ctg ttg ttc agc 576  
 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser  
 180 185 190

5 gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc 624  
 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr  
 195 200 205

10 tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg 672  
 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr  
 210 215 220

15 cgc agc ctg gct ttg cat cca gcc ctc tct ttc gca gct tgt tac aac 720  
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn  
 225 230 235 240

20 ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt 768  
 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe  
 245 250 255

cag ctg cca caa ctt cga aat gaa tca ttc act tga 804  
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<211> 267

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<213> Artificial variant

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Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala  
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Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu  
 35 40 45

50

Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu  
 50 55 60

5 Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu  
 65 70 75 80  
 Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His  
 85 90 95  
 10 Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala  
 100 105 110  
 15 Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Gly  
 115 120 125  
 20 His Pro Gly Thr Asp Leu Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn  
 130 135 140  
 25 Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met  
 145 150 155 160  
 Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu  
 165 170 175  
 30 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser  
 180 185 190  
 35 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr  
 195 200 205  
 40 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr  
 210 215 220  
 45 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn  
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 1 5 10 15  
 ctt tat att gat ata tcc caa ttc aag ttt tgg atg ttg tta ccg ctc 96  
 Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu  
 30 20 25 30  
 ata ttt tgg caa aca ttt tta tat acg gga tta ttt att aca gct cat 144  
 Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
 35 35 40 45  
 gat gcc atg cat ggg gta gtt ttt ccc aaa aat ccc aaa atc aac cat 192  
 Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His  
 50 55 60  
 40 ttc att ggc tca ttg tgc ctg ttt ctt tat ggt ctt tta cct tat caa 240  
 Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln  
 65 70 75 80  
 aaa ctt tta aaa aag cat tgg cta cat cac cat aat cca gcc agt gaa 288  
 45 Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu  
 85 90 95  
 aca gat cca gat ttt cac aac ggg aag cag aaa aac ttt ttt gct tgg 336  
 Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp  
 50 100 105 110  
 tat tta tat ttt atg aag cgt tac tgg agt tgg tta caa att atc aca 384

Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr  
 115 120 125

5 tta atg att att tat aac tta cta aaa tat ata tgg cat ttt cca gag 432  
 Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu  
 130 135 140

10 gat aat atg act tat ttt tgg gta gtt ccc tca att tta agt tct tta 480  
 Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu  
 145 150 155 160

15 caa tta ttt tat ttt gga act ttt cta ccc cac agt gag cct gta gaa 528  
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu  
 165 170 175

ggt tat aaa gag cct cat cgt tcc caa act att agc cgt ccc att tgg 576  
 Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp  
 180 185 190

20 tgg tca ttt ata act tgt tac cat ttt ggt tat cat tac gaa cat cat 624  
 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His  
 195 200 205

25 gaa tac ccc cat gtt cct tgg tgg caa tta cca gaa att tat aaa atg 672  
 Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met  
 210 215 220

30 tct aaa tca aat ttg tga 690  
 Ser Lys Ser Asn Leu  
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40 <213> Nodularia spumigena NSOR10

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 20 25 30

Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
 35 40 45

5 Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His  
 50 55 60

10 Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln  
 65 70 75 80

15 Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu  
 85 90 95

Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp  
 100 105 110

20 Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr  
 115 120 125

25 Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu  
 130 135 140

30 Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu  
 145 150 155 160

35 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu  
 165 170 175

Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp  
 180 185 190

40 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His  
 195 200 205

45 Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met  
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50 Ser Lys Ser Asn Leu  
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gcgcatgctc tagactatgt tgctttgtaa atttctg 37

50 <210> 56  
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20 1 5 10 15

gca aaa ctg act cca gta ctg aga agt aaa tct cag ttt aag ggg ctt , 97  
Ala Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu  
20 25 30

25

ttc att gct att gtc att gtt agc gca tgg gtc att agc ctg agt tta 145  
Phe Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu  
35 40 45

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tta ctt tcc ctt gac atc tca aag cta aaa ttt tgg atg tta ttg cct 193  
Leu Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro  
50 55 60

35

ggt ata cta tgg caa aca ttt tta tat acg gga tta ttt att aca tct 241  
Val Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser  
65 70 75

40

cat gat gcc atg cat ggc gta gta ttt ccc caa aac acc aag att aat 289  
His Asp Ala Met His Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn  
80 85 90 95

cat ttg att gga aca ttg acc cta tcc ctt tat ggt ctt tta cca tat 337  
His Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr  
100 105 110

45

caa aaa cta ttg aaa aaa cat tgg tta cac cac cac aat cca gca agc 385  
Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser  
115 120 125

50

tca ata gac ccg gat ttt cac aat ggt aaa cac caa agt ttc ttt gct 433  
Ser Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala  
130 135 140

|    |   |     |
|----|---|-----|
|    | tgg tat ttt cat ttt atg aaa ggt tac tgg agt tgg ggg caa ata att | 481 |
|    | Trp Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile |     |
|    | 145 150 155   |     |
| 5  | gcg ttg act att att tat aac ttt gct aaa tac ata ctc cat atc cca | 529 |
|    | Ala Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro |     |
|    | 160 165 170 175   |     |
| 10 | agt gat aat cta act tac ttt tgg gtg cta ccc tcg ctt tta agt tca | 577 |
|    | Ser Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser |     |
|    | 180 185 190   |     |
| 15 | tta caa tta ttc tat ttt ggt act ttt tta ccc cat agt gaa cca ata | 625 |
|    | Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile |     |
|    | 195 200 205   |     |
| 20 | ggg ggt tat gtt cag cct cat tgt gcc caa aca att agc cgt cct att | 673 |
|    | Gly Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile |     |
|    | 210 215 220   |     |
| 25 | tgg tgg tca ttt atc acg tgc tat cat ttt ggc tac cac gag gaa cat | 721 |
|    | Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His |     |
|    | 225 230 235   |     |
| 30 | cac gaa tat cct cat att tct tgg tgg cag tta cca gaa att tac aaa | 769 |
|    | His Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys |     |
|    | 240 245 250 255   |     |
| 35 | gca aaa tagtctagag catgcgc                                      | 792 |
|    | Ala Lys   |     |
| 40 | <210> 57  |     |
|    | <211> 257   |     |
|    | <212> PRT   |     |
|    | <213> Nostoc punctiforme ATCC 29133                             |     |
| 45 | <400> 57  |     |
|    | Met His Leu Glu Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala |     |
|    | 1 5 10 15   |     |
| 50 | Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe |     |
|    | 20 25 30  |     |

Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu  
35 40 45

5

Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val  
50 55 60

10

Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His  
65 70 75 80

15

Asp Ala Met His Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His  
.85 .90 .95

20

Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln  
100 105 110

25

Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Ser  
115 120 125

30

Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp  
130 135 140

35

Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala  
145 150 155 160

40

Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser  
165 170 175

45

Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu  
180 185 190

50

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly  
195 200 205

55

Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp  
210 215 220

60

Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His  
225 230 235 240

Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala  
245 250 255

5

Lys

10

&lt;210&gt; 58

&lt;211&gt; 26

15

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

20

&lt;220&gt;

&lt;221&gt; Primer

25

&lt;222&gt; (1)..(26)

&lt;223&gt;

30

&lt;400&gt; 58

gtcgacâctg ctttaatgag atatgc

26

35

&lt;210&gt; 59

&lt;211&gt; 27

&lt;212&gt; DNA

40

&lt;213&gt; Artificial sequence

45

&lt;220&gt;

&lt;221&gt; Primer

&lt;222&gt; (1)..(27)

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&lt;223&gt;

5 <400> 59  
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10 <210> 60  
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 <213> Agrobacterium tumefaciens

15 <220>  
 <221> Terminator  
 <222> (1)..(210)  
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 30 ttctgtttgtg cacgttgtaa aaaacctgag catgtgtagc tcagatcctt accgccggtt 120  
 tcggttcatt ctaatgaata tatcaccctg tactatcgta tttttatgaa taatattctc 180  
 35 cgttcaattt actgattgtc caagctcgag 210

40 <210> 61  
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45 <220>  
 <221> Primer  
 50 <222> (1)..(37)

&lt;223&gt;

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37

10 <210> 62

&lt;211&gt; 38

&lt;212&gt; DNA

15 <213> Artificial sequence

20 <220>

&lt;221&gt; Primer

&lt;222&gt; (1)..(38)

25 <223>

30 <400> 62  
aagcttggtt gatcagaaga agaagaagaa gatgaact

38

&lt;210&gt; 63

35 <211> 652

&lt;212&gt; DNA

40 <213> Arabidopsis thaliana

&lt;220&gt;

45 <221> Promoter

&lt;222&gt; (1)..(652)

50 <223>

<400> 63  
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 ttgtgtaata ctttaccctg gttaatcaaa aacaaaaagg cttttgagct tttttagtt 120  
 5 gaatttctct ggctgatctt ttctgtacag attcatatat ctgcagagac gatatcattg 180  
 attatttgag cttcttttga actatttcgt gtaatttggg atgagagctc tatgtatgtg 240  
 10 tgtaaacttt gaagacaaca agaaaggtaa caagtgaggg agggatgact ccatgtcaaa 300  
 atagatgtca taagaggccc atcaataagt gcttgagccc attagctagc ccagtaacta 360  
 ccagattgtg agatggatgt gtgaacagtt ttttttttga tgtaggactg aaatgtgaac 420  
 15 aacaggcgca tgaaaggcta aattaggaca atgataagca gaaataactt atcctctcta 480  
 acacttgccc tcacattgcc cttcacacaa tccacacaca tccaatcaca acctcatcat 540  
 20 atatctcccg ctaatctttt tttctttgat cttttttttt ttgcttatta tttttttgac 600  
 tttgatctcc catcagttca tcttcttctt cttcttctga tcaaccaagc tt 652  
  
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 30 <213> Artificial sequence  
  
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<212> DNA

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<222> (1)..(29)

<223>

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<210> 66

<211> 1773

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<212> DNA

<213> Petunia hybrida

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<220>

<221> Promoter

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<222> (1)..(1773)

<223>

40

<400> 66

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45

catttggtta ctctctgctg tggtagttgg catatccaca ttgtctcctt ccacttttat 180

gacaattacg tgaaagttat gggttgtttt gtctattttt gtcgaggcct ttcttttcct 240

50

tccaggttgt tgaagatggt ccaattcgat tagaataatg ttttgagctt tagcatattc 300

tctctcgttt acacgattat agtaataatg atataggatg acagaagttg acacataaat 360



tttttattct ctccatttac tttaatccaa atctcaccta ccctaaactt ctttaatatg 420  
 tattcaatag tctatccgag taaattgtaa atttaacaac cattgataat attgacacct 480  
 5 actaacatat actagtaaag agaattattaa catggcacat ataatttgat gcaaaatgag 540  
 tatgatgaaa tttaaaccce aaatctcttg attttgacag tgtcaccttg acttggttaac 600  
 10 taataagtca tgtttttagtg gcagaaagac aaactcatcc accaactgta tagcaataaa 660  
 aaatagaaga atcttcctga ggcaaagttt tggaaaaatt aagagtggct gagatttaat 720  
 ttcaacagga attagttcca cttaactttt aggttacgat acagtgctaa tttaataact 780  
 15 taattgtatt agatatttct tgcacctaaa aaatttaaaa actgaaaaaa ggtagcaatc 840  
 aaaataaaca aaaggacaaa ataagtgaag ggtacagcca ccaaccctgg cggctcactg 900  
 20 tttgttggtt aaaacgtaga cttacaccta ccaaaatcta caactaaaat gaggcaataa 960  
 tactttgccc aaaattacca agaaaagaaa aagaaaggaa tcccttaata ttactctcct 1020  
 ccatttcaca ataaatatcc tagtttgact taaattagag tttaaaaaat gaaagacgac 1080  
 25 ttttaaaact tgtaatctaa aataaatcat agttaaatgt gtggctataa atcattgtat 1140  
 taacggtaaa gtggttaagt taaaagttaa ttgttttcaa atataaaatt gtactatcat 1200  
 30 tctttttgga atggactaat aagaaaacta tgacatccat tatggagcgg agggagtatc 1260  
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 tattattgat gttaagtacc acatcatcct taatgataga atcatcgtag aacgcttttc 1380  
 35 caggcacaca ttcaaactag ttagaccagt accacacatc gaatattcca gacttctttg 1440  
 tttgaatagt cgactacatt ggataatgga acttctcgaa ttaacttcga attagtcgag 1500  
 40 cccaaaataa tatatacgtc ggttggaata ctataaaatg ttgacaaaa atgtcaaatt 1560  
 aatatatcaa tctgcaacaa ctttttcacc ttgagaacac agctgaaatt ttttacaag 1620  
 gtagttggtg aagctagtca gcgaatccca ttaccttcca ctctacctaa ccccttcac 1680  
 45 caacaacaaa tttctgtaat ttaaaaacta gccaaaaaag aactctcttt tacaagagc 1740  
 caaagactca atctttactt tcaagaaaag ctt 1773  
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<211> 39

<212> DNA

5 <213> Artificial sequence

<220>

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<221> Primer

<222> (1)..(39)

15

<223>

<400> 67

20 gcgcacatgcac ctacaaatga atttttgtga taaaccagt

39

<210> 68

25

<211> 37

<212> DNA

<213> Artificial sequence

30

<220>

35

<221> Primer

<222> (1)..(37)

<223>

40

<400> 68

45 gcgcacatgctc tagattacga attgggttact gaattgt

37

<210> 69

50

<211> 819

<212> DNA

&lt;213&gt; Nostoc punctiforme ATCC 29133

5 &lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5)..(802)

10

&lt;223&gt;

15

&lt;400&gt; .69

gcgc atg cat cta gaa atg aat ttt tgt gat aaa cca gtt agc tat tat 49  
 Met His Leu Glu Met Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr  
 1 5 10 15

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gtt gca ata gag caa tta agt gct aaa gaa gat act gtt tgg ggg ctg 97  
 Val Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu  
 20 25 30

25

gtg att gtc ata gta att att agt ctt tgg gta gct agt ttg gct ttt 145  
 Val Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe  
 35 40 45

30

tta cta gct att aat tat gcc aaa gtc cca att tgg ttg ata cct att 193  
 Leu Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile  
 50 55 60

35

gca ata gtt tgg caa atg ttc ctt tat aca ggg cta ttt att act gca 241  
 Ala Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala  
 65 70 75

cat gat gct atg cat ggg tca gtt tat cgt aaa aat ccc aaa att aat 289  
 His Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn  
 80 85 90 95

40

aat ttt atc ggt tca cta gct gta gcg ctt tac gct gtg ttt cca tat 337  
 Asn Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr  
 100 105 110

45

caa cag atg tta aag aat cat tgc tta cat cat cgt cat cct gct agc 385  
 Gln Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser  
 115 120 125

50

gaa gtt gac cca gat ttt cat gat ggt aag aga aca aac gct att ttc 433  
 Glu Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe  
 130 135 140

tgg tat ctc cat ttc atg ata gaa tac tcc agt tgg caa cag tta ata 481

Trp Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile  
 145 150 155

5 gta cta act atc cta ttt aat tta gct aaa tac gtt ttg cac atc cat 529  
 Val Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His  
 160 165 170 175

10 caa ata aat ctc atc tta ttt tgg agt att cct cca att tta agt tcc 577  
 Gln Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser  
 180 185 190

15 att caa ctg ttt tat ttc gga aca ttt ttg cct cat cga gaa ccc aag 625  
 Ile Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys  
 195 200 205

aaa gga tat gtt tat ccc cat tgc agc caa aca ata aaa ttg cca act 673  
 Lys Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr  
 210 215 220

20 ttt ttg tca ttt atc gct tgc tac cac ttt ggt tat cat gaa gaa cat 721  
 Phe Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His  
 225 230 235

25 cat gag tat ccc cat gta cct tgg tgg caa ctt cca tct gta tat aag 769  
 His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys  
 240 245 250 255

30 cag aga gta ttc aac aat tca gta acc aat tcg taatctagag catgcgc 819  
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 260 265

<210> 70

35 <211> 266

<212> PRT

40 <213> Nostoc punctiforme ATCC 29133

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45 Met His Leu Glu Met Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val  
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50 Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val  
 20 25 30

Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu  
 35 40 45

5 Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala  
 50 55 60

10 Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
 65 70 75 80

15 Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn  
 85 90 95

Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln  
 100 105 110

20 Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser Glu  
 115 120 125

25 Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp  
 130 135 140

30 Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val  
 145 150 155 160

35 Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln  
 165 170 175

Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile  
 180 185 190

40 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys  
 195 200 205

45 Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe  
 210 215 220

50 Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His  
 225 230 235 240

Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln  
245 250 255

5 Arg Val Phe Asn Asn Ser Val Thr Asn Ser  
260 265

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<211> 33

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15 <213> Artificial sequence

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20 <221> Primer

<222> (1)..(33)

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33

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35 <211> 32

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<222> (1)..(32)

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&lt;400&gt; 72

gcgc atg cat cta gaa atg gcg atc gcc att att agt ata tgg gct atc

32

5 &lt;210&gt; 73

&lt;211&gt; 720

&lt;212&gt; DNA

10

&lt;213&gt; Nodularia spumigena NSOR10

15 &lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5)..(703)

20

&lt;223&gt;

25 &lt;400&gt; 73

gcgc atg cat cta gaa atg gcg atc gcc att att agt ata tgg gct atc  
 Met His Leu Glu Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile  
 1 5 10 15

49

30 agc cta ggt ttg tta ctt tat att gat ata tcc caa ttc aag ttt tgg  
 Ser Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp  
 20 25 30

97

35 atg ttg tta ccg ctc ata ttt tgg caa aca ttt tta tat acg gga tta  
 Met Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu  
 35 40 45

145

40 ttt att aca gct cat gat gcc atg cat ggg gta gtt ttt ccc aaa aat  
 Phe Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn  
 50 55 60

193

45 ccc aaa atc aac cat ttc att ggc tca ttg tgc ctg ttt ctt tat ggt  
 Pro Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly  
 65 70 75

241

50 ctt tta cct tat caa aaa ctt tta aaa aag cat tgg cta cat cac cat  
 Leu Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His  
 80 85 90 95

289

50 aat cca gcc agt gaa aca gat cca gat ttt cac aac ggg aag cag aaa  
 Asn Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys  
 100 105 110

337

aac ttt ttt gct tgg tat tta tat ttt atg aag cgt tac tgg agt tgg 385  
 Asn Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp  
 115 120 125

5

tta caa att atc aca tta atg att att tat aac tta cta aaa tat ata 433  
 Leu Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile  
 130 135 140

10

tgg cat ttt cca gag gat aat atg act tat ttt tgg gta gtt ccc tca 481  
 Trp His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser  
 145 150 155

15

att tta agt tct tta caa tta ttt tat ttt gga act ttt cta ccc cac 529  
 Ile Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His  
 160 165 170 175

20

agt gag cct gta gaa ggt tat aaa gag cct cat cgt tcc caa act att 577  
 Ser Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile  
 180 185 190

25

agc cgt ccc att tgg tgg tca ttt ata act tgt tac cat ttt ggt tat 625  
 Ser Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr  
 195 200 205

30

cat tac gaa cat cat gaa tac ccc cat gtt cct tgg tgg caa tta cca 673  
 His Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro  
 210 215 220

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gaa att tat aaa atg tct aaa tca aat ttg tgatctagag catgcgc 720  
 Glu Ile Tyr Lys Met Ser Lys Ser Asn Leu  
 225 230

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<210> 74  
 <211> 233  
 <212> PRT  
 <213> Nodularia spumigena NSOR10

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<400> 74  
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50

Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met  
 20 25 30



5 Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe  
     35                    40                    45

10 Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro  
     50                    55                    60

15 Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu  
     65                    70                    75                    80

20 Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn  
                     85                    90                    95

25 Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn  
                     100                    105                    110

30 Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu  
                     115                    120                    125

35 Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp  
     130                    135                    140

40 His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile  
     145                    150                    155                    160

45 Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser  
                     165                    170                    175

50 Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser  
                     180                    185                    190

Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His  
                     195                    200                    205

Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu  
     210                    215                    220

Ile Tyr Lys Met Ser Lys Ser Asn Leu  
     225                    230